



1600

RAW SEQUENCE LISTING

DATE: 02/24/2003 P6

PATENT APPLICATION: US/09/515,363C

TIME: 13:44:43

Input Set : A:\#427587 v1 - A34614 Sequence Listing.txt

Output Set: N:\CRF4\02242003\I515363C.raw

```

4 <110> APPLICANT: Fisher, Paul B.
5      Kang, Dong-Chul
6      Gopalkrishnan, Rahul V.
8 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED
9      GENE-5 AND PROMOTER AND USES THEREOF
12 <130> FILE REFERENCE: A34614 (070050.1690)
15 <140> CURRENT APPLICATION NUMBER: 09/515,363C
16 <141> CURRENT FILING DATE: 2000-02-29
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3365
24 <212> TYPE: DNA
25 <213> ORGANISM: homo sapiens
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29 cctgcttctc taagtgggca gcggacagcg gcacgcacat ttcacctgic ccgcagacaa 120
30 cagcaccatc tgcttgggag aacctctctc ctctctctgag aaagaaaagat gtcgaatggg 180
31 tattccacag acgagaattt ccgctatctc atctcgtgct tcagggccag ggtgaaaatg 240
32 tacatccagg tggagcctgt gctggactac ctgacctttc tgccctgcaga ggtgaaggag 300
33 cagattcaga ggacagtcgc cacctccggg aacatgcagg cagttgaact gctgctgagc 360
34 accttgga gaaggagtctg gcaccttggg tggactcggg aattcgtgga ggccctccgg 420
35 agaaccggca gccctctggc cggccctctc atgaacctg agctcacgga cttgccctct 480
36 ccctcgtttg agaacgctca tgatgaatat ctccaactgc tgaacctcct tcagccact 540
37 ctggtggaca agcttctagt tagagacgtc ttggataagt gcatggagga ggaactgttg 600
38 acaattgaag acagaaaccg gattgctgct gcagaaaaca atggaaatga atcaggtgta 660
39 agagagctac taaaaaggat tgtgcagaaa gaaaactggt tctctgcatt tctgaatgtt 720
40 ctctgtcaaa caggaaacaa tgaacttgct caagagttaa caggctctga ttgctcagaa 780
41 agcaatgcag agattgagaa tttatcacaa gttgatggtc ctcaagtgga agagcaactt 840
42 ctttcaacca cagttcagcc aaatctggag aaggaggtct ggggcattgga gaataactca 900
43 tcagaatcat ctittgcaga ttcttctgta gtttcagaat cagacacaag tttggcagaa 960
44 ggaagtgtca gctgcttaga tgaaaactct ggacataaca gcaacatggg cagtgttca 1020
45 ggcaccatgg gaagtgtatc agatgaagag aatgtggcag caagagcatc cccggagcca 1080
46 gaactccagc tcaggcccta ccaaaatgaa gttgccagc cagccttggg agggagaagt 1140
47 atcatcatct gccctctac agggagtggg aaaaccagag tggctgttta cattgccaa 1200
48 gatcacttag acaagaagaa aaaagcatct gagcctggaa aagttatagt tcttgtcaat 1260
49 aaggtactgc tagttgaaca gctcttccgc aaggagtcc aaccattttt gaagaaatgg 1320
50 tatcgtgtta ttggattaag tgggtgatac caactgaaaa tatcatttcc agaagttgtc 1380
51 aagtcctgtg atattattat cagtacagct caaatccttg aaaactccct cttaaacttg 1440
52 gaaaatggag aagatgctgg tgttcaattg tcagactttt ccttcattat cattgatgaa 1500
53 tgtcatcaca ccaacaaaag agcagtgtat aataacatca tgaggcatta ttgatgcag 1560
54 aagttgaaaa acaatagact caagaaagaa aacaaaccag tgattccctt tcttcagata 1620
55 ctgggactaa cagcttcacc tgggtgttga ggggccacga agcaagccaa agctgaagaa 1680

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56 cacatttttaa aactatgtgc caatcttgat gcattttacta ttaaaactgt taaagaaaac 1740
57 ctgtatcaac tgaaaaacca aatacaggag ccattgcaaga agtttgccat tgcagatgca 1800
58 accagagaag atccatttaa agagaaactt ctagaaataa tgacaaggat tcaaacttat 1860
59 tgtcaaatga gtccaatgtc agatttttggg actcaaccct atgaacaatg ggccattcaa 1920
60 atggaaaaaaa aagctgcaaa aaaaggaaat cgcaagaac gtgtttgtgc agaacatttg 1980
61 aggaagtaca atgaggccct acaaattaat gacacaatc gaatgataga tgcgtatact 2040
62 catcttgaaa ctttctataa tgaagagaaa gataagaagt ttgcagtcac agaagatgat 2100
63 agtgatgagg gtggtgatga tgagtattgt gatggtgatg aagatgagga tgatttaaag 2160
64 aaacctttga aactggatga aacagataga tttctcatga ctttattttt tgaaaaaca 2220
65 aaaaattgtga aaaggctggc tgaaaacca gaatatgaaa atgaaaagct gaccaaaata 2280
66 agaaatacca taatggagca atatactagg actgaggaat cagcacgagg aataatcttt 2340
67 acaaaaacac gacagagtc atatgcgctt tcccagtgga ttactgaaaa tgaaaaattt 2400
68 gctgaagtag gagtcaaagc ccaccatctg attggagctg gacacagcag tgagttcaaa 2460
69 cccatgacac agaatgaaca aaaagaagtc attagtaaat ttgcactgg aaaaatcaat 2520
70 ctgcttatcg ctaccacagt ggcagaagaa ggtctggata ttaaagaatg taacattgtt 2580
71 atccgttatg gtctcgtcac caatgaaata gccatggtcc aggccctgg tcgagccaga 2640
72 gctgatgaga gcacctacgt cctggttgct cacagtgggt caggagtat cgaacatgag 2700
73 acagttaatg atttccgaga gaagatgatg tataaagcta tacatttgtt tcaaaatatg 2760
74 aaaccagagg agtatgctca taagattttg gaattacaga tgcaaagtat aatggaaaag 2820
75 aaaatgaaaa ccaagagaaa tatggccaag cattaacaaga ataaccatc actaataact 2880
76 ttccctttgca aaaactgcag tgtgctagcc tgttctgggg aagatatcca tgtaattgag 2940
77 aaaatgcac acgtcaatat gacccagaa ttcaaggaac ttacattgt aagagaaaac 3000
78 aaagcactgc aaaagaagtg tgcgactat caaataaatg gtgaaatcat ctgcaaagt 3060
79 ggccaggctt ggggaacaat gatggtgcac aaaggcttag atttgccttg tctcaaaata 3120
80 aggaattttg tagtggtttt caaaaataa tcaacaaaga aacaatacaa aaagtgggta 3180
81 gaattacctc tcacatttcc caatcttgac tattcagaat gctgtttatt tagtgatgag 3240
82 gattgacctg tgattgaaga ttcttttaaa atactatcag ttaaacattt aatatgatta 3300
83 tgattaatgt attcattatg ctacagaact gacataagaa tcaataaaat gattgtttta 3360
84 ctctg 3365

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86 <210> SEQ ID NO: 2

87 <211> LENGTH: 1025

88 <212> TYPE: PRT

89 <213> ORGANISM: homo sapiens

91 <400> SEQUENCE: 2

```

92 Met Ser Asn Gly Tyr Ser Thr Asp Glu Asn Phe Arg Tyr Leu Ile Ser
93 1 5 10 15
94 Cys Phe Arg Ala Arg Val Lys Met Tyr Ile Gln Val Glu Pro Val Leu
95 20 25 30
96 Asp Tyr Leu Thr Phe Leu Pro Ala Glu Val Lys Glu Gln Ile Gln Arg
97 35 40 45
98 Thr Val Ala Thr Ser Gly Asn Met Gln Ala Val Glu Leu Leu Leu Ser
99 50 55 60
100 Thr Leu Glu Lys Gly Val Trp His Leu Gly Trp Thr Arg Glu Phe Val
101 65 70 75 80
102 Glu Ala Leu Arg Arg Thr Gly Ser Pro Leu Ala Ala Arg Tyr Met Asn
103 85 90 95
104 Pro Glu Leu Thr Asp Leu Pro Ser Pro Ser Phe Glu Asn Ala His Asp
105 100 105 110
106 Glu Tyr Leu Gln Leu Leu Asn Leu Leu Gln Pro Thr Leu Val Asp Lys

```

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107	115	120	125
108	Leu Leu Val Arg Asp Val Leu Asp Lys Cys Met Glu Glu Glu Leu Leu		
109	130	135	140
110	Thr Ile Glu Asp Arg Asn Arg Ile Ala Ala Ala Glu Asn Asn Gly Asn		
111	145	150	155
112	Glu Ser Gly Val Arg Glu Leu Leu Lys Arg Ile Val Gln Lys Glu Asn		
113	165	170	175
114	Trp Phe Ser Ala Phe Leu Asn Val Leu Arg Gln Thr Gly Asn Asn Glu		
115	180	185	190
116	Leu Val Gln Glu Leu Thr Gly Ser Asp Cys Ser Glu Ser Asn Ala Glu		
117	195	200	205
118	Ile Glu Asn Leu Ser Gln Val Asp Gly Pro Gln Val Glu Glu Gln Leu		
119	210	215	220
120	Leu Ser Thr Thr Val Gln Pro Asn Leu Glu Lys Glu Val Trp Gly Met		
121	225	230	235
122	Glu Asn Asn Ser Ser Glu Ser Ser Phe Ala Asp Ser Ser Val Val Ser		
123	245	250	255
124	Glu Ser Asp Thr Ser Leu Ala Glu Gly Ser Val Ser Cys Leu Asp Glu		
125	260	265	270
126	Ser Leu Gly His Asn Ser Asn Met Gly Ser Asp Ser Gly Thr Met Gly		
127	275	280	285
128	Ser Asp Ser Asp Glu Glu Asn Val Ala Ala Arg Ala Ser Pro Glu Pro		
129	290	295	300
130	Glu Leu Gln Leu Arg Pro Tyr Gln Met Glu Val Ala Gln Pro Ala Leu		
131	305	310	315
132	Glu Gly Lys Asn Ile Ile Cys Leu Pro Thr Gly Ser Gly Lys Thr		
133	325	330	335
134	Arg Val Ala Val Tyr Ile Ala Lys Asp His Leu Asp Lys Lys Lys Lys		
135	340	345	350
136	Ala Ser Glu Pro Gly Lys Val Ile Val Leu Val Asn Lys Val Leu Leu		
137	355	360	365
138	Val Glu Gln Leu Phe Arg Lys Glu Phe Gln Pro Phe Leu Lys Lys Trp		
139	370	375	380
140	Tyr Arg Val Ile Gly Leu Ser Gly Asp Thr Gln Leu Lys Ile Ser Phe		
141	385	390	395
142	Pro Glu Val Val Lys Ser Cys Asp Ile Ile Ile Ser Thr Ala Gln Ile		
143	405	410	415
144	Leu Glu Asn Ser Leu Leu Asn Leu Glu Asn Gly Glu Asp Ala Gly Val		
145	420	425	430
146	Gln Leu Ser Asp Phe Ser Leu Ile Ile Asp Glu Cys His His Thr		
147	435	440	445
148	Asn Lys Glu Ala Val Tyr Asn Asn Ile Met Arg His Tyr Leu Met Gln		
149	450	455	460
150	Lys Leu Lys Asn Asn Arg Leu Lys Lys Glu Asn Lys Pro Val Ile Pro		
151	465	470	475
152	Leu Pro Gln Ile Leu Gly Leu Thr Ala Ser Pro Gly Val Gly Gly Ala		
153	485	490	495
154	Thr Lys Gln Ala Lys Ala Glu Glu His Ile Leu Lys Leu Cys Ala Asn		
155	500	505	510

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```

156 Leu Asp Ala Phe Thr Ile Lys Thr Val Lys Glu Asn Leu Asp Gln Leu
157      515      520      525
158 Lys Asn Gln Ile Gln Glu Pro Cys Lys Lys Phe Ala Ile Ala Asp Ala
159      530      535      540
160 Thr Arg Glu Asp Pro Phe Lys Glu Lys Leu Leu Glu Ile Met Thr Arg
161 545      550      555      560
162 Ile Gln Thr Tyr Cys Gln Met Ser Pro Met Ser Asp Phe Gly Thr Gln
163      565      570      575
164 Pro Tyr Glu Gln Trp Ala Ile Gln Met Glu Lys Lys Ala Ala Lys Lys
165      580      585      590
166 Gly Asn Arg Lys Glu Arg Val Cys Ala Glu His Leu Arg Lys Tyr Asn
167      595      600      605
168 Glu Ala Leu Gln Ile Asn Asp Thr Ile Arg Met Ile Asp Ala Tyr Thr
169      610      615      620
170 His Leu Glu Thr Phe Tyr Asn Glu Glu Lys Asp Lys Lys Phe Ala Val
171 625      630      635      640
172 Ile Glu Asp Asp Ser Asp Glu Gly Gly Asp Asp Glu Tyr Cys Asp Gly
173      645      650      655
174 Asp Glu Asp Glu Asp Asp Leu Lys Lys Pro Leu Lys Leu Asp Glu Thr
175      660      665      670
176 Asp Arg Phe Leu Met Thr Leu Phe Phe Glu Asn Asn Lys Met Leu Lys
177      675      680      685
178 Arg Leu Ala Glu Asn Pro Glu Tyr Glu Asn Glu Lys Leu Thr Lys Leu
179      690      695      700
180 Arg Asn Thr Ile Met Glu Gln Tyr Thr Arg Thr Glu Glu Ser Ala Arg
181 705      710      715      720
182 Gly Ile Ile Phe Thr Lys Thr Arg Gln Ser Ala Tyr Ala Leu Ser Gln
183      725      730      735
184 Trp Ile Thr Glu Asn Glu Lys Phe Ala Glu Val Gly Val Lys Ala His
185      740      745      750
186 His Leu Ile Gly Ala Gly His Ser Ser Glu Phe Lys Pro Met Thr Gln
187      755      760      765
188 Asn Glu Gln Lys Glu Val Ile Ser Lys Phe Arg Thr Gly Lys Ile Asn
189      770      775      780
190 Leu Leu Ile Ala Thr Thr Val Ala Glu Glu Gly Leu Asp Ile Lys Glu
191 785      790      795      800
192 Cys Asn Ile Val Ile Arg Tyr Gly Leu Val Thr Asn Glu Ile Ala Met
193      805      810      815
194 Val Gln Ala Arg Gly Arg Ala Arg Ala Asp Glu Ser Thr Tyr Val Leu
195      820      825      830
196 Val Ala His Ser Gly Ser Gly Val Ile Glu His Glu Thr Val Asn Asp
197      835      840      845
198 Phe Arg Glu Lys Met Met Tyr Lys Ala Ile His Cys Val Gln Asn Met
199      850      855      860
200 Lys Pro Glu Glu Tyr Ala His Lys Ile Leu Glu Leu Gln Met Gln Ser
201 865      870      875      880
202 Ile Met Glu Lys Lys Met Lys Thr Lys Arg Asn Ile Ala Lys His Tyr
203      885      890      895
204 Lys Asn Asn Pro Ser Leu Ile Thr Phe Leu Cys Lys Asn Cys Ser Val

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```

205          900          905          910
206 Leu Ala Cys Ser Gly Glu Asp Ile His Val Ile Glu Lys Met His His
207          915          920          925
208 Val Asn Met Thr Pro Glu Phe Lys Glu Leu Tyr Ile Val Arg Glu Asn
209          930          935          940
210 Lys Ala Leu Gln Lys Lys Cys Ala Asp Tyr Gln Ile Asn Gly Glu Ile
211 945          950          955          960
212 Ile Cys Lys Cys Gly Gln Ala Trp Gly Thr Met Met Val His Lys Gly
213          965          970          975
214 Leu Asp Leu Pro Cys Leu Lys Ile Arg Asn Phe Val Val Val Phe Lys
215          980          985          990
216 Asn Asn Ser Thr Lys Lys Gln Tyr Lys Lys Trp Val Glu Leu Pro Ile
217          995          1000          1005
218 Thr Phe Pro Asn Leu Asp Tyr Ser Glu Cys Cys Leu Phe Ser Asp Glu
219          1010          1015          1020

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220 Asp

221 1025

224 <210> SEQ ID NO: 3

225 <211> LENGTH: 1036

226 <212> TYPE: DNA

227 <213> ORGANISM: homo sapiens

229 <220> FEATURE:

230 <221> NAME/KEY: misc_feature

231 <222> LOCATION: 551

232 <223> OTHER INFORMATION: n = A,T,C or G

234 <400> SEQUENCE: 3

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235 gcacattttg gacctacaaag gaccttattg ttaaggcaga acctgctggg aaaacaaaat 60
236 atccgccgga ggagctttgt agagcgttgg tcttggtgtc agagagaatt cgctttcctt 120
237 ttctgtttcc cgcggtgtcc ttaaccaaag gctcctcttc ttacccgcc cgcacaaaaa 180
238 ggtggcgtct cctgaggaa actccctccc cgcaggcag attacgttta caaagtcctg 240
239 agaagagaat cgaacacagaa accaaagtca ggcaactct gtaagaactg cctgacagaa 300
240 agctggactc aaagctccta cccgagtgtg cagcaggatc gccccggtcc gggacccccag 360
241 gcgcacaccg cagagtccaa agtgccgcgc ctgccggccg cacctgcctg ccgcggcccc 420
242 gcgcgcgcgc ccgctgcccc cctgcccgcc tgcccacctg ccaggtgcg agtgcagccc 480
243 cgcgcgcgcg cctgagagcc ctgtggacaa cctcgtcatt gtcaggcaca gacgggtaga 540
W--> 244 ccctgcttct ntaagtgggc agcggacagc ggcacgcaca ttacacctgt ccgcagaca 600
245 acagcaccat ctgcttggga gaacctctc ccttctctga gaaagaaaga tgtcgatgg 660
246 gtattccaca gacgagaatt tccgctatct catctcgtgc ttcagggccca gggtgaaaat 720
247 gtacatccag gtggagcctg tgctggacta cctgaccttt ctgcctgcag aggtgaagga 780
248 gcagattcag aggacagtcg ccacctccgg gaacatgcag gcagttgaac tgctgctgag 840
249 caccttggag aaggagctct ggcaccttgg ttggactcgg gaattcgtgg aggcctccg 900
250 gagaaccggc agcctcttgg ccgccgcta catgaacct gagctcagc acttgccctc 960
251 tccatcgttt gagaacgctc atgatgaata tctccaactg ctgaacctcc ttcagcccac 1020
252 tctggtggac aagctt                                     1036

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254 <210> SEQ ID NO: 4

255 <211> LENGTH: 202

256 <212> TYPE: DNA

257 <213> ORGANISM: homo sapiens

259 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/515,363C

DATE: 02/24/2003
TIME: 13:44:44

Input Set : A:\#427587 v1 - A34614 Sequence Listing.txt
Output Set: N:\CRF4\02242003\I515363C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 551
Seq#:4; N Pos. 33,73,107
Seq#:17; Xaa Pos. 8,9
Seq#:19; Xaa Pos. 1,2,3,5
Seq#:22; Xaa Pos. 3
Seq#:23; Xaa Pos. 6,7

VERIFICATION SUMMARY

DATE: 02/24/2003

PATENT APPLICATION: US/09/515,363C

TIME: 13:44:44

Input Set : A:\#427587 v1 - A34614 Sequence Listing.txt

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L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:540
L:268 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:272 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:341 Repeated in SeqNo=4
L:609 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:613 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:617 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:643 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:647 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:651 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:655 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:659 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:698 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:702 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:715 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:719 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:723 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0